

RESEARCH LETTERS

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Household Transmission of Human Adenovirus Type 55 in Case of Fatal Acute Respiratory Disease

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DOI: <https://doi.org/10.3201/eid2509.181937>

We identified a case of fatal acute respiratory disease from household transmission of human adenovirus type 55 (HAdV-55) in Anhui Province, China. Computed tomography showed severe pneumonia. Comparative genomic analysis of HAdV-55 indicated the virus possibly originated in Shanxi Province, China. More attention should be paid to highly contagious HAdV-55.

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Human adenoviruses are associated with mild and acute respiratory infections, depending on the virus type and host immunity. Human adenovirus type 55 (HAdV-55) (1), formerly known as HAdV-11a (2), is a reemergent respiratory pathogen that has caused severe pneumonia outbreaks in military and civilian populations in Europe and Asia (2–7). However, household transmission of HAdV-55 is rarely reported. We report a case of household transmission of HAdV-55 involving 3 confirmed adult cases with 1 death. Epidemiologic, clinical, and laboratory investigations, along with whole-genome sequencing, elucidate the disease progression and the pathogen origin.

During April 1–May 5, 2012, 7 household members (5 males and 2 females; 3 children and 4 adults) in Anhui Province, China, sequentially experienced influenza-like symptoms, including fever, productive cough, fatigue, pharyngalgia, dyspnea, and other symptoms. The youngest patient was 4 months of age, the oldest, whom we refer to as AQ-1, was a 55-year-old man. The family lived together near a farm in a house with poor sanitary and ventilation conditions.

The first onset of acute respiratory disease (ARD) occurred on April 1, when the index case, a 4-year-old granddaughter of AQ-1, had a febrile respiratory infection with cough. Three days later, AQ-1's grandson, 1 year of age, displayed similar symptoms. On April 9 and 11, AQ-1's daughter, 28 years of age, and another grandson, 4 months of age, both had influenza-like symptoms. On April 14, AQ-1 had a fever, chills, and lumbago. He was admitted to the hospital on April 14 where clinicians diagnosed pneumonia. AQ-1 had close contact with his sick grandsons and granddaughter and had not been out of the house during the month he cared for them.

While hospitalized, AQ-1 had bilateral pneumonia seen on chest computed tomography (CT), a temperature of 41.0°C, and low total leukocyte ($3.63 \times 10^9/L$) and platelet ($42 \times 10^9/L$) counts. AQ-1 sustained high fever and yellow phlegm despite antiinflammatory and antiviral treatment, including levofloxacin, piperacillin sodium, tazobactam sodium, and ribavirin.

On April 24, AQ-1 had indications of severe pneumonia, including respiratory failure, hypoxemia, double lung rales, and a mass of shadows visible on chest CT. In addition, he had indications of liver damage and multi-organ failure. Transverse chest CT images demonstrated increased areas of patchy shadows and consolidation in both lungs compared to CT images from April 22, indicative of disease progression (Appendix Figure 1, <http://wwwnc.cdc.gov/EID/article/25/9/18-1937-App1.pdf>).

AQ-1 died on April 27, 3 days after onset of respiratory failure, and 13 days after his illness began. On the same day, his 20-year-old son, AQ-2, and 31-year-old nephew, AQ-3, who had taken care of AQ-1 for 5 days, also exhibited

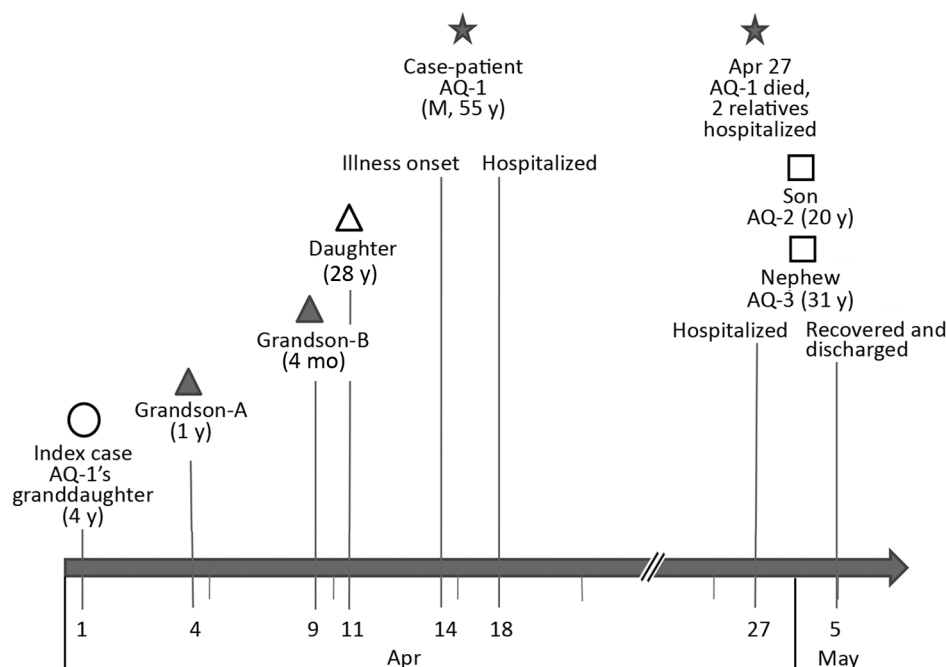


Figure. Timeline of patients' illness onset in a household cluster of acute respiratory disease from human adenovirus 55, Anhui Province, China, 2012. The star indicates AQ-1, the case described in this study. Case relationships to AQ-1 are indicated along with their ages at the date of their illness onset.

symptoms of influenza-like illness. Both were hospitalized and had normal chest CT scans, but AQ-2's leukocyte count was $5.4 \times 10^9/L$ and AQ-3's was $6.7 \times 10^9/L$. After antiinflammatory and antiviral treatment, including vitamin C, sulbactam, amoxicillin, amikacin, cefoperazone, ribavirin, and oseltamivir, they recovered and were discharged on May 5 (Figure).

We tested endotracheal aspirates from AQ-1 and throat swabs from AQ-2 and AQ-3 for influenza A and B viruses, severe acute respiratory syndrome coronavirus, human metapneumovirus, rhinoviruses, parainfluenza viruses 1–4, and HAdVs by real-time PCR. Only adenovirus was strongly positive for all 3 patients. Testing for antibodies against *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Treponema pallidum*, hepatitis B and C viruses, and HIV were all negative. After treatment, samples from AQ-2 and AQ-3, were negative for adenovirus by PCR.

We isolated AQ-1's adenovirus in culture and sequenced the genome (GenBank accession no. KP279748). Sequences for the hexon, penton base, and fiber genes were identical to those previously reported for HAdV-55. Phylogenetic analysis showed that the 3 isolates clustered closely with other strains from China (Appendix Figure 2). The genome of AQ-1's strain had the highest nucleotide identity (99.951%) with QZ01_2011, an isolate from a military trainee in Shanxi Province, China. The second highest identity (99.948%) was with QS-DLL_2006, which caused a fatal ARD outbreak in a senior high school in Shaanxi Province, China (1,8) (Appendix Table). We hypothesize the strain infecting AQ-1 and his family originated from Shanxi Province.

In this household transmission of ARD, the index case was a probable case because no specimens were collected to confirm virologic identification. From the timeline of illness onset in this household cluster of ARD cases (Figure), we suspect that the pathogen spread rapidly among the children and further circulated in adults who had close contact with infected children and one another.

HAdV-55 contains a 97.4% genome of HAdV-14 and a hexon from HAdV-11 (1). Since 2006, HAdV-14 has caused severe ARD in America, Europe, and Asia (8,9), with high hospitalization (38%) and case-fatality (5%) rates (10). Because the risk for infection among the close contacts may rise, more attention should be paid to these highly contagious pathogens.

This study was approved by the institutional review board of Anqing Center for Disease Control and Prevention and was supported by the National Natural Science Foundation of China (grant nos. 31570155, 31370199, 81730061, 81471942) and Guangzhou Healthcare Collaborative Innovation Major Project (grant nos. 201803040004, 201803040007).

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Worldwide Reduction in MERS Cases and Deaths since 2016

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DOI: <https://doi.org/10.3201/eid2509.190143>

Since 2012, Middle East respiratory syndrome (MERS) coronavirus has infected 2,442 persons worldwide. Case-based data analysis suggests that since 2016, as many as 1,465 cases and 293–520 deaths might have been averted. Efforts to reduce the global MERS threat are working, but countries must maintain vigilance to prevent further infections.

From 2012 through May 31, 2019, Middle East respiratory syndrome coronavirus (MERS-CoV) has infected 2,442 persons and killed 842 worldwide (1). MERS-CoV is currently circulating in dromedary camels in Africa, the Middle East, and southern Asia; however, most cases of human infection have been reported in the Arabian Peninsula (2). Large hospital outbreaks in 2014 and 2015 (3,4) (Appendix Figure 1, <https://wwwnc.cdc.gov/EID/article/25/9/19-0143-F1.htm>) motivated affected countries to substantially invest in prevention and control activities.

To estimate the potential number of MERS cases and deaths that might have been averted since 2016 had the risk levels of 2014–2015 continued, we analyzed case-based data on laboratory-confirmed human cases of MERS-CoV infections reported to the World Health Organization (5). We categorized cases as either secondary (human-to-human transmission) or community-acquired (presumed camel-to-human transmission). In addition, we used case-based data on date of onset (for symptomatic infections) or report (for asymptomatic infections), outcome (died/recovered), and dates and sizes of reported clusters of human-to-human transmission cases (3,4,6–8).

We compared incidence of camel-to-human transmission cases (i.e., community-acquired cases, assuming all of those not positively attributed to human-to-human transmission were in this category) during 2016, 2017, and 2018 (through September only) with incidence during 2014–2015, assuming that case numbers were Poisson distributed